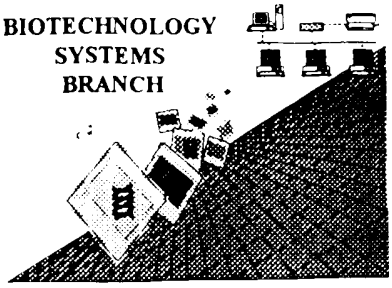
BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/743,247

Source: PCT/09

Date Processed by STIC: 8/3/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/743,247

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1	Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2	Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.
3	Misaligned Amino Numbering	The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
4	Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
5	Variable Length	Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6	PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
7	Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
8	Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000
9	Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
10	Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
11	Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
12	PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
13	Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

PCT09

RAW SEQUENCE LISTING DATE: 08/03/2001
PATENT APPLICATION: US/09/743,247 TIME: 16:29:03

Input Set : A:\ES.txt
Output Set: N:\CRF3\08032001\I743247.raw

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      3 <110> APPLICANT: Sagami Chemical Research Center; Protegene Inc.
      5 <120> TITLE OF INVENTION: Human Proteins Having Hydrophobic Domains And DNAs Encoding
These
      6       Proteins
      8 <130> FILE REFERENCE: 661102
C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/743,247
C--> 10 <141> CURRENT FILING DATE: 1999-07-22
     10 <150> PRIOR APPLICATION NUMBER: JP 10-208820
     11 <151> PRIOR FILING DATE: 1998-07-24
     13 <150> PRIOR APPLICATION NUMBER: JP 10-224105
     14 <151> PRIOR FILING DATE: 1998-08-07
     16 <150> PRIOR APPLICATION NUMBER: JP 10-238116
     17 <151> PRIOR FILING DATE: 1998-08-25
     19 <150> PRIOR APPLICATION NUMBER: JP 10-254736
     20 <151> PRIOR FILING DATE: 1998-09-09
     22 <150> PRIOR APPLICATION NUMBER: JP 10-275505
     23 <151> PRIOR FILING DATE: 1998-09-29
     25 <160> NUMBER OF SEQ ID NOS: 150
     27 <170> SOFTWARE: Windows 95 (Word 98)
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1-5

ERRORED SEQUENCES

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    519 <210> SEQ ID NO: 21
    520 <211> LENGTH: 510
    521 <212> TYPE: DNA
    522 <213> ORGANISM: Homo sapiens
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    524 <221> NAME/KEY: CDS
    525 <222> LOCATION: (66)...(443)
    527 <400> SEQUENCE: 21
    528 acgcttgatc cccggccgcg gggccaggaa gtcggagttt gagccccgga ggcagagcgg     60
    529 ctgcc atg gcc aag tac ctg gcc cag atc att gtg atg ggc gtg cag gtg    110
    530       Met Ala Lys Tyr Leu Ala Gln Ile Ile Val Met Gly Val Gln Val
    531         1               5                  10                  15
    532 gtg ggc agg gcc ttt gca cgg gcc ttg cgg cag gag ttt gca gcc agc      158
    533 Val Gly Arg Ala Phe Ala Arg Ala Leu Arg Gln Glu Phe Ala Ala Ser
    534                 20                  25                  30
    535 cgg gcc gca gct gat gcc cga gga cgc gct gga cac cgg tct gca gcc      206
    536 Arg Ala Ala Ala Asp Ala Arg Gly Arg Ala Gly His Arg Ser Ala Ala
    537             35                  40                  45
    538 gct tcc aac ctc tcc ggc ctc agc ctc cag gag gca cag cag att ctc      254
    539 Ala Ser Asn Leu Ser Gly Leu Ser Leu Gln Glu Ala Gln Gln Ile Leu
    540          50                  55                  60
    541 aac gtg tcc aag ctg agc cct gag gag gtc cag aag aac tat gaa cac      302
    542 Asn Val Ser Lys Leu Ser Pro Glu Glu Val Gln Lys Asn Tyr Glu His
    543      65                  70                  75
    544 tta ttt aag gtg aat gat aaa tcc gtg ggt ggc tcc ttc tac ctg cag      350
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RAW SEQUENCE LISTING DATE: 08/03/2001
PATENT APPLICATION: US/09/743,247 TIME: 16:29:03

Input Set : A:\ES.txt
Output Set: N:\CRF3\08032001\I743247.raw

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     545 Leu Phe Lys Val Asn Asp Lys Ser Val Gly Gly Ser Phe Tyr Leu Gln
     546  80                  85                  90                  95
     547 tca aag gtg gtc cgc gca aag gag cgc ctg gat gag gaa ctc aaa atc      398
     548 Ser Lys Val Val Arg Ala Lys Glu Arg Leu Asp Glu Glu Leu Lys Ile
     549                 100                 105                 110
E--> 550 cag gcc cag gag gac aga gaa aaa ggg cag atg ccc cat acg tgactgctc   (450) 449
     551 Gln Ala Gln Glu Asp Arg Glu Lys Gly Gln Met Pro His Thr
     552             115                 120                 125
E--> 553 gctccccccg cccaccccgc cgcctctaat ttatagcttg gtaataaatt tcttttctgc   (510) SC9
     3553 <210> SEQ ID NO: 93
     3554 <211> LENGTH: 195
     3555 <212> TYPE: PRT
     3556 <213> ORGANISM: Homo sapience
     3558 <400> SEQUENCE: 93
     3559 Met Arg Leu Leu Leu Leu Leu Leu Val Ala Ala Ser Ala Met Val Arg
     3560   1               5                  10                  15
     3561 Ser Glu Ala Ser Ala Asn Leu Gly Gly Val Pro Ser Lys Arg Leu Lys
     3562              20                  25                  30
     3563 Met Gln Tyr Ala Thr Gly Pro Leu Leu Lys Phe Gln Ile Cys Val Ser
     3564          35                  40                  45
E--> 3565 Xaa Gly Tyr Arg Arg Val Phe Glu Glu Tyr Met Arg Val Ile Ser Gln
     3566      50                  55                  60
     3567 Arg Tyr Pro Asp Ile Arg Ile Glu Gly Glu Asn Tyr Leu Pro Gln Pro
     3568  65                  70                  75                  80
     3569 Ile Tyr Arg His Ile Ala Ser Phe Leu Ser Val Phe Lys Leu Val Leu
     3570                  85                  90                  95
     3571 Ile Gly Leu Ile Ile Val Gly Lys Asp Pro Phe Ala Phe Phe Gly Met
     3572              100                 105                 110
     3573 Gln Ala Pro Ser Ile Trp Gln Trp Gly Gln Glu Asn Lys Val Tyr Ala
     3574          115                 120                 125
     3575 Cys Met Met Val Phe Phe Leu Ser Asn Met Ile Glu Asn Gln Cys Met
     3576      130                 135                 140
     3577 Ser Thr Gly Ala Phe Glu Ile Thr Leu Asn Asp Val Pro Val Trp Ser
     3578 145                 150                 155                 160
     3579 Lys Leu Glu Ser Gly His Leu Pro Ser Met Gln Gln Leu Val Gln Ile
     3580                 165                 170                 175
     3581 Leu Asp Asn Glu Met Lys Leu Asn Val His Met Asp Ser Ile Pro His
     3582              180                 185                 190
     3583 His Arg Ser
     3584          195
     4525 <210> SEQ ID NO: 116
     4526 <211> LENGTH: 1357
     4527 <212> TYPE: DNA
     4528 <213> ORGANISM: Homo Sapience
W--> 4529 <220> FEATURE:
     4530 <221> NAME/KEY: CDS
     4531 <222> LOCATION: (81)...(1262)
     4533 <400> SEQUENCE: 116
     4534 cgtgcgtttg tggccgtccg gcctccctga catgcagccc tctggacccc gaggttggac      60
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RAW SEQUENCE LISTING DATE: 08/03/2001
PATENT APPLICATION: US/09/743,247 TIME: 16:29:04

Input Set : A:\ES.txt
Output Set: N:\CRF3\08032001\I743247.raw

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4535 cctactgtga cacacctacc atg cgg aca ctc ttc aac ctc ctc tgg ctt      110
4536                       Met Arg Thr Leu Phe Asn Leu Leu Trp Leu
4537                         1               5                  10
4538 gcc ctg gcc tgc agc cct gtt cac act acc ctg tca aag tca gat gcc      158
4539 Ala Leu Ala Cys Ser Pro Val His Thr Thr Leu Ser Lys Ser Asp Ala
4540                 15                  20                  25
E--> 4541 aaa aaa gcc gcc tca aag acg ctg ctg gag aag agt cag ttt tca gat  203
4542 Lys Lys Ala Ala Ser Lys Thr Leu Leu Glu Lys Ser Gln Phe Ser Asp
4543              30                  35                  40
4544 aag ccg gtg caa gac cgg ggt ttg gtg gtg acg gac ctc aaa gct gag      254
4545 Lys Pro Val Gln Asp Arg Gly Leu Val Val Thr Asp Leu Lys Ala Glu
4546          45                  50                  55
4547 agt gtg gtt ctt gag cat cgc agc tac tgc tcg gca aag gcc cgg gac      302
4548 Ser Val Val Leu Glu His Arg Ser Tyr Cys Ser Ala Lys Ala Arg Asp
4549      60                  65                  70
4550 aga cac ttt gct ggg gat gta ctg ggc tat gtc act cca tgg aac agc      350
4551 Arg His Phe Ala Gly Asp Val Leu Gly Tyr Val Thr Pro Trp Asn Ser
4552  75                  80                  85                  90
4553 cat ggc tac gat gtc acc aag gtc ttt ggg agc aag ttc aca cag atc      398
4554 His Gly Tyr Asp Val Thr Lys Val Phe Gly Ser Lys Phe Thr Gln Ile
4555                 95                 100                 105
4556 tca ccc gtc tgg ctg cag ctg aag aga cgt ggc cgt gag atg ttt gag      446
4557 Ser Pro Val Trp Leu Gln Leu Lys Arg Arg Gly Arg Glu Met Phe Glu
4558              110                 115                 120
4559 gtc acg ggc ctc cac gac gtg gac caa ggg tgg atg cga gct gtc agg      494
4560 Val Thr Gly Leu His Asp Val Asp Gln Gly Trp Met Arg Ala Val Arg
4561          125                 130                 135
4562 aag cat gcc aag ggc ctg cac ata gtg cct cgg ctc ctg ttt gag gac      542
4563 Lys His Ala Lys Gly Leu His Ile Val Pro Arg Leu Leu Phe Glu Asp
4564      140                 145                 150
4565 tgg act tac gat gat ttc cgg aac gtc tta gac agt gag gat gag ata      590
4566 Trp Thr Tyr Asp Asp Phe Arg Asn Val Leu Asp Ser Glu Asp Glu Ile
4567 155                 160                 165                 170
4568 gag gag ctg agc aag acc gtg gtc cag gtg gca aag aac cag cat ttc      638
4569 Glu Glu Leu Ser Lys Thr Val Val Gln Val Ala Lys Asn Gln His Phe
4570                 175                 180                 185
4571 gat ggc ttc gtg gtg gag gtc tgg aac cag ctg cta agc cag aag cgc      686
4572 Asp Gly Phe Val Val Glu Val Trp Asn Gln Leu Leu Ser Gln Lys Arg
4573              190                 195                 200
4574 gtg ggc ctc atc cac atg ctc acc cac ttg gcc gag gct ctg cac cag      734
4575 Val Gly Leu Ile His Met Leu Thr His Leu Ala Glu Ala Leu His Gln
4576          205                 210                 215
4577 gcc cgg ctg ctg gcc ctc ctg gtc atc ccg cct gcc atc acc ccc ggg      782
4578 Ala Arg Leu Leu Ala Leu Leu Val Ile Pro Pro Ala Ile Thr Pro Gly
4579      220                 225                 230
4580 acc gac cag ctg ggc atg ttc acg cac aag gag ttt gag cag ctg gcc      830
4581 Thr Asp Gln Leu Gly Met Phe Thr His Lys Glu Phe Glu Gln Leu Ala
4582 235                 240                 245                 250
4583 ccc gtg ctg gat ggt ttc agc ctc atg acc tac gac tac tct aca gcg      878
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RAW SEQUENCE LISTING DATE: 08/03/2001
PATENT APPLICATION: US/09/743,247 TIME: 16:29:04

Input Set : A:\ES.txt
Output Set: N:\CRF3\08032001\I743247.raw

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4584 Pro Val Leu Asp Gly Phe Ser Leu Met Thr Tyr Asp Tyr Ser Thr Ala
4585                 255                 260                 265
4586 cat cag cct ggc cct aat gca ccc ctg tcc tgg gtt cga gcc tgc gtc      926
4587 His Gln Pro Gly Pro Asn Ala Pro Leu Ser Trp Val Arg Ala Cys Val
4588             270                 275                 280
4589 cag gtc ctg gac ccg aag tcc aag tgg cga agc aaa atc ctc ctg ggg      974
4590 Gln Val Leu Asp Pro Lys Ser Lys Trp Arg Ser Lys Ile Leu Leu Gly
4591         285                 290                 295
4592 ctc aac ttc tat ggt atg gac tac gcg acc tcc aag gat gcc cgt gag     1022
4593 Leu Asn Phe Tyr Gly Met Asp Tyr Ala Thr Ser Lys Asp Ala Arg Glu
4594     300                 305                 310
4595 cct gtt gtc ggg gcc agg tac atc cag aca ctg aag gac cac agg ccc     1070
4596 Pro Val Val Gly Ala Arg Tyr Ile Gln Thr Leu Lys Asp His Arg Pro
4597 315                 320                 325                 330
4598 cgg atg gtg tgg gac agc cag gcc tca gag cac ttc ttc gag tac aag     1118
4599 Arg Met Val Trp Asp Ser Gln Ala Ser Glu His Phe Phe Glu Tyr Lys
4600                 335                 340                 345
4601 aag agc cgc agt ggg agg cac gtc gtc ttc tac cca acc ctg aag tcc     1166
4602 Lys Ser Arg Ser Gly Arg His Val Val Phe Tyr Pro Thr Leu Lys Ser
4603             350                 355                 360
4604 ctg cag gtg cgg ctg gag ctg gcc cgg gag ctg ggc gtt ggg gtc tct     1214
4605 Leu Gln Val Arg Leu Glu Leu Ala Arg Glu Leu Gly Val Gly Val Ser
4606         365                 370                 375
4607 atc tgg gag ctg ggc cag ggc ctg gac tac ttc tac gac ctg ctc t       1260
4608 Ile Trp Glu Leu Gly Gln Gly Leu Asp Tyr Phe Tyr Asp Leu Leu
4609     380                 385                 390
4610 aggtgggcat tgcggcctcc gcggtggacg tgttcttttc taagccatgg agtgagtgag   1320
4611 caggtgtgaa atacaggcct ccactccgtt tgctgtg                          1357
5735 <210> SEQ ID NO: 144
5736 <211> LENGTH: 619
5737 <212> TYPE: DNA
5738 <213> ORGANISM: Homo sapience
W--> 5739 <220> FEATURE:
5740 <221> NAME/KEY: CDS
5741 <222> LOCATION: (13)...(333)
5743 <400> SEQUENCE: 144
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5745                Met Ser Thr Asn Asn Met Ser Asp Pro Arg Arg Pro
5746                  1               5                  10
5747 aac aaa gtg ctg agg tac aag ccc ccg ccg agc gaa tgt aac ccg gcc       96
5748 Asn Lys Val Leu Arg Tyr Lys Pro Pro Pro Ser Glu Cys Asn Pro Ala
5749          15                  20                  25
5750 ttg gac gac ccg acg ccg gac tac atg aac ctg ctg ggc atg atc ttc      144
5751 Leu Asp Asp Pro Thr Pro Asp Tyr Met Asn Leu Leu Gly Met Ile Phe
5752      30                  35                  40
5753 agc atg tgc ggc ctc atg ctt aag ctg aag tgg tgt gct tgg gtc gct      192
5754 Ser Met Cys Gly Leu Met Leu Lys Leu Lys Trp Cys Ala Trp Val Ala
5755  45                  50                  55                  60
5756 gtc tac tgc tcc ttc atc agc ttt gcc aac tct cgg agc tcg gag gac      240
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RAW SEQUENCE LISTING DATE: 08/03/2001
PATENT APPLICATION: US/09/743,247 TIME: 16:29:04

Input Set : A:\ES.txt
Output Set: N:\CRF3\08032001\I743247.raw

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5757 Val Tyr Cys Ser Phe Ile Ser Phe Ala Asn Ser Arg Ser Ser Glu Asp
5758                 65                  70                  75
5759 acg aag caa atg atg agt agc ttc atg ctg tcc atc tct gcc gtg gtg      288
5760 Thr Lys Gln Met Met Ser Ser Phe Met Leu Ser Ile Ser Ala Val Val
5761              80                  85                  90
E--> 5762 atg tcc tat ctg cag aat cct cag ccc atg acg ccc cca tgg        340
5763 Met Ser Tyr Leu Gln Asn Pro Gln Pro Met Thr Pro Pro Trp
5764          95                  100                 105
5765 tgataccagc ctagaagggt cacattttgg accctgtcta tccactaggc ctgggctttg    390
5766 gctgctaaac ctgctgcctt cagctgccat cctggacttc cctgaatgag gccgtctcgg    450
5767 tgcccccagc tggatagagg gaacctggcc ctttcctagg gaacacccta ggcttacccc    510
5768 tcctgcctcc cttcccctgc ctgctgctgg gggagatgct gtccatgttt ctaggggtat    570
5769 tcatttgctt tctcgttgaa acctgttgtt aataaagttt ttcactcag              619
5976 <210> SEQ ID NO: 149
5977 <211> LENGTH: 2182
5978 <212> TYPE: DNA
5979 <213> ORGANISM: Homo sapience
W--> 5980 <220> FEATURE:
5981 <221> NAME/KEY: CDS
5982 <222> LOCATION: (56)...(1090)
5984 <400> SEQUENCE: 149
E--> 5985 gcacttcagc ttcccctccc ccggcgccct ctggggctcc gagcccggcg ggacc      58
5986 atg ttc acc agc acc ggc tcc agt ggg ctc tac aag gcg cct ctg tcg      103
5987 Met Phe Thr Ser Thr Gly Ser Ser Gly Leu Tyr Lys Ala Pro Leu Ser
5988   1               5                  10                  15
5989 aag agc ctt ctg ctg gtc ccc agt gcc ctc tcc ctc ctg ctc gcc ctc      151
5990 Lys Ser Leu Leu Leu Val Pro Ser Ala Leu Ser Leu Leu Leu Ala Leu
5991              20                  25                  30
5992 ctc ctg cct cac tgc cag aag ctc ttt gtg tat gac ctt cac gca gtc      199
5993 Leu Leu Pro His Cys Gln Lys Leu Phe Val Tyr Asp Leu His Ala Val
5994          35                  40                  45
5995 aag aac gac ttc cag att tgg agg ttg ata tgt gga aga ata att tgc      247
5996 Lys Asn Asp Phe Gln Ile Trp Arg Leu Ile Cys Gly Arg Ile Ile Cys
5997      50                  55                  60
5998 ctt gat ttg aaa gat act ttc tgc agt agt ctg ctt att tat aat ttt      295
5999 Leu Asp Leu Lys Asp Thr Phe Cys Ser Ser Leu Leu Ile Tyr Asn Phe
6000  65                  70                  75                  80
6001 agg ata ttt gaa aga aga tat gga agc aga aaa ttt gca tcc ttt ttg      343
6002 Arg Ile Phe Glu Arg Arg Tyr Gly Ser Arg Lys Phe Ala Ser Phe Leu
6003                  85                  90                  95
6004 ctg ggt tcc tgg gtt ttg tca gcc tta ttt gac ttt ctc ctc att gaa      391
6005 Leu Gly Ser Trp Val Leu Ser Ala Leu Phe Asp Phe Leu Leu Ile Glu
6006              100                 105                 110
6007 gct atg cag tat ttc ttt ggc atc act gca gct agt aat ttg cct tct      439
6008 Ala Met Gln Tyr Phe Phe Gly Ile Thr Ala Ala Ser Asn Leu Pro Ser
6009          115                 120                 125
6010 gga ttc ctg gca cct gtg ttt gct ctg ttt gta cca ttt tac tgc tcc      487
6011 Gly Phe Leu Ala Pro Val Phe Ala Leu Phe Val Pro Phe Tyr Cys Ser
6012      130                 135                 140
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RAW SEQUENCE LISTING DATE: 08/03/2001
PATENT APPLICATION: US/09/743,247 TIME: 16:29:05

Input Set : A:\ES.txt
Output Set: N:\CRF3\08032001\I743247.raw

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6013 ata cca aga gtc caa gtg gca caa att ctg ggt ccg ttg tcc atc aca      535
6014 Ile Pro Arg Val Gln Val Ala Gln Ile Leu Gly Pro Leu Ser Ile Thr
6015 145                 150                 155                 160
6016 aac aag aca ttg att tat ata ttg gga ctg cag ctt ttc acc tct ggt      583
6017 Asn Lys Thr Leu Ile Tyr Ile Leu Gly Leu Gln Leu Phe Thr Ser Gly
6018                 165                 170                 175
6019 tcc tac atc tgg att gta gcc ata agt gga ctt atg tcc ggt ctg tgc      631
6020 Ser Tyr Ile Trp Ile Val Ala Ile Ser Gly Leu Met Ser Gly Leu Cys
6021             180                 185                 190
6022 tac gac agc aaa atg ttc cag gtg cat cag gtg ctc tgc atc ccc agc      679
6023 Tyr Asp Ser Lys Met Phe Gln Val His Gln Val Leu Cys Ile Pro Ser
6024         195                 200                 205
6025 tgg atg gca aaa ttc ttt tct tgg aca ctt gaa ccc atc ttc tct tct      727
6026 Trp Met Ala Lys Phe Phe Ser Trp Thr Leu Glu Pro Ile Phe Ser Ser
6027     210                 215                 220
6028 tca gaa ccc acc agc gaa gcc aga att ggg atg gga gcc acg ctg gac      775
6029 Ser Glu Pro Thr Ser Glu Ala Arg Ile Gly Met Gly Ala Thr Leu Asp
6030 225                 230                 235                 240
6031 atc cag aga cag cag aga atg gag ctg ctg gac cgg cag ctg atg ttc      823
6032 Ile Gln Arg Gln Gln Arg Met Glu Leu Leu Asp Arg Gln Leu Met Phe
6033                 245                 250                 255
6034 tct cag ttt gca caa ggg agg cga cag aga cag cag cag gga gga atg      871
6035 Ser Gln Phe Ala Gln Gly Arg Arg Gln Arg Gln Gln Gln Gly Gly Met
6036             260                 265                 270
6037 atc aat tgg aat cgt ctt ttt cct cct tta cgt cag cga caa aac gta      919
6038 Ile Asn Trp Asn Arg Leu Phe Pro Pro Leu Arg Gln Arg Gln Asn Val
6039         275                 280                 285
6040 aac tat cag ggc ggt cgg cag tct gag cca gca gcg ccc cct cta gaa      967
6041 Asn Tyr Gln Gly Gly Arg Gln Ser Glu Pro Ala Ala Pro Pro Leu Glu
6042     290                 295                 300
6043 gtt tct gag gaa cag gtc gcc cgg ctc atg gag atg gga ttt tcc aga     1015
6044 Val Ser Glu Glu Gln Val Ala Arg Leu Met Glu Met Gly Phe Ser Arg
6045 305                 310                 315                 320
6046 ggt gat gct ttg gaa gcc ctg aga gct tca aac aat gac ctc aat gtc     1063
6047 Gly Asp Ala Leu Glu Ala Leu Arg Ala Ser Asn Asn Asp Leu Asn Val
6048                 325                 330                 335
6049 gcc acc aac ttc ctg ctg cag cac tgatagtccc aggccaacac tgg           1110
6050 Ala Thr Asn Phe Leu Leu Gln His
6051             340
6052 gaccggaccg gcagccgagt gacagtgcgt ggtccccacc atcagatcag cccggggacc   1170
6053 gagcatctct ggtgctgatg ttcttgtggg aagagggagg ttccaccgca cccctgccct   1230
6054 caaccgcaag actgttgccg ttttagtgtg gagataagtt tgccattaca ttagcatgta   1290
6055 ttttctatct atatttttta ttgggcattt tccctaggtt ggagagtcag cactcgtttt   1350
6056 gaatgtgttt aaaatgcatt aaaatggaag atttctgcag gcagttgaat ggcactccag   1410
6057 atggggaatt gctgtaaccc tcttactgta acatgtcatc tcctgcgtcg tgatggggag   1470
6058 agggtaatgt tacttcacaa aggacatgtc agatccttct tcatggactt ttttagttac   1530
6059 tgttttttct ctcaaacttg ttttcgaatc tcctgggagt gagggagaaa cagggagctg   1590
6060 aatcctcccc caagctgttc caggccagag gactctgcag taccttctcc tacatctagt   1650
6061 aacaaagaat ggtgataacc atgcactggt tcaaggttct ggagttctcc atgaaacttg   1710
```

RAW SEQUENCE LISTING DATE: 08/03/2001
PATENT APPLICATION: US/09/743,247 TIME: 16:29:05

Input Set : A:\ES.txt
Output Set: N:\CRF3\08032001\I743247.raw

6062 ggttaatttt gctcagagta tccggagtta gccactaggc tgcgggtgaa atgggatgga 1770
6063 gtagaacaac agcaggcttc ctggagccac atgggctgac tagggcactc tgtggctggc 1830
6064 ctggcacggg ctcagcccag gaagaggaga aacgatccct tgcctgcccc tccctgtggc 1890
6065 agggctaact gcctggccct cctggctcgc agccagccag ccccctggca gcaggttctc 1950
6066 ctcagggctt gggtcttcaa cctgtggcga caggaggcag ggcagactgt ggaggacagg 2010
6067 atgcaggtca gggagaggga aggcaggggt ggaccgccat gagcatgaaa agacccgaag 2070
6068 caagttgact cttgcaatgt gcaactgtta tgttctgcaa aatgagcaac gatgtatcaa 2130
6069 attgatgcaa atttagatgt tgatacttac aataaagttt ttaatgtgtt tt 2182

VERIFICATION SUMMARY DATE: 08/03/2001
PATENT APPLICATION: **US/09/743,247** TIME: 16:29:06

Input Set : **A:\ES.txt**
Output Set: **N:\CRF3\08032001\I743247.raw**

L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:523 M:283 W: Missing Blank Line separator, <220> field identifier
L:550 M:254 E: No. of Bases conflict, LENGTH:Input:450 Counted:449 SEQ:21
M:254 Repeated in SeqNo=21
L:553 M:252 E: No. of Seq. differs, <211>LENGTH:Input:510 Found:509 SEQ:21
L:559 M:283 W: Missing Blank Line separator, <220> field identifier
L:601 M:283 W: Missing Blank Line separator, <220> field identifier
L:674 M:283 W: Missing Blank Line separator, <220> field identifier
L:740 M:283 W: Missing Blank Line separator, <220> field identifier
L:778 M:283 W: Missing Blank Line separator, <220> field identifier
L:827 M:283 W: Missing Blank Line separator, <220> field identifier
L:888 M:112 C: (48) String data converted to lower case,
L:910 M:283 W: Missing Blank Line separator, <220> field identifier
L:946 M:283 W: Missing Blank Line separator, <220> field identifier
L:986 M:283 W: Missing Blank Line separator, <220> field identifier
L:1618 M:283 W: Missing Blank Line separator, <220> field identifier
L:1690 M:283 W: Missing Blank Line separator, <220> field identifier
L:1749 M:283 W: Missing Blank Line separator, <220> field identifier
L:1853 M:283 W: Missing Blank Line separator, <220> field identifier
L:1889 M:283 W: Missing Blank Line separator, <220> field identifier
L:1942 M:283 W: Missing Blank Line separator, <220> field identifier
L:2025 M:283 W: Missing Blank Line separator, <220> field identifier
L:2085 M:283 W: Missing Blank Line separator, <220> field identifier
L:2121 M:283 W: Missing Blank Line separator, <220> field identifier
L:2169 M:283 W: Missing Blank Line separator, <220> field identifier
L:2780 M:283 W: Missing Blank Line separator, <220> field identifier
L:2858 M:283 W: Missing Blank Line separator, <220> field identifier
L:2911 M:283 W: Missing Blank Line separator, <220> field identifier
L:2997 M:283 W: Missing Blank Line separator, <220> field identifier
L:3057 M:283 W: Missing Blank Line separator, <220> field identifier
L:3099 M:283 W: Missing Blank Line separator, <220> field identifier
L:3189 M:283 W: Missing Blank Line separator, <220> field identifier
L:3227 M:283 W: Missing Blank Line separator, <220> field identifier
L:3373 M:283 W: Missing Blank Line separator, <220> field identifier
L:3412 M:283 W: Missing Blank Line separator, <220> field identifier
L:3565 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:93
L:4104 M:283 W: Missing Blank Line separator, <220> field identifier
L:4192 M:283 W: Missing Blank Line separator, <220> field identifier
L:4270 M:283 W: Missing Blank Line separator, <220> field identifier
L:4285 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:113
L:4285 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:113
L:4332 M:283 W: Missing Blank Line separator, <220> field identifier
L:4414 M:283 W: Missing Blank Line separator, <220> field identifier
L:4529 M:283 W: Missing Blank Line separator, <220> field identifier
L:4541 M:254 E: No. of Bases conflict, LENGTH:Input:203 Counted:206 SEQ:116
L:4617 M:283 W: Missing Blank Line separator, <220> field identifier
L:4668 M:283 W: Missing Blank Line separator, <220> field identifier

VERIFICATION SUMMARY DATE: 08/03/2001
PATENT APPLICATION: **US/09/743,247** TIME: 16:29:06

Input Set : **A:\ES.txt**
Output Set: **N:\CRF3\08032001\I743247.raw**

L:4705 M:283 W: Missing Blank Line separator, <220> field identifier
L:4788 M:283 W: Missing Blank Line separator, <220> field identifier
L:5453 M:283 W: Missing Blank Line separator, <220> field identifier
L:5566 M:283 W: Missing Blank Line separator, <220> field identifier
L:5670 M:283 W: Missing Blank Line separator, <220> field identifier
L:5739 M:283 W: Missing Blank Line separator, <220> field identifier
L:5762 M:254 E: No. of Bases conflict, LENGTH:Input:340 Counted:330 SEQ:144
L:5775 M:283 W: Missing Blank Line separator, <220> field identifier
L:5833 M:283 W: Missing Blank Line separator, <220> field identifier
L:5906 M:283 W: Missing Blank Line separator, <220> field identifier
L:5945 M:283 W: Missing Blank Line separator, <220> field identifier
L:5980 M:283 W: Missing Blank Line separator, <220> field identifier
L:5985 M:254 E: No. of Bases conflict, LENGTH:Input:58 Counted:55 SEQ:149
L:6075 M:283 W: Missing Blank Line separator, <220> field identifier